

OM of: us-09-972-467-2_COPY_289_478 to: GenEmbl:* out_format : pfs
Date: Jun 20, 2002 6:50 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:
-MODEL:frame+p2n.model -DEV=xlh
-0=/con2-1/ruspto.spool/rus9972467/runat_20062002_105946_2165/app_query.fasta_1.2455
-DB=GenEmbl -QPM=fastap -SUFFIX=large -GAPOP=12.000 -GAPEXT=4.000
-OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELETE=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=50 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0
-ALIGN=25 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=200000000 -USER=us09972467@cgml1_13316
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1

Arch information block:
Merry length: 190

Database: GenEmbl:
Database sequences: 1797656
Database length: 187333701
Search time (sec): 7733.930000

score_list:

Sequence	Strd	Orig	Zscore	Escore	Len	Documentation
gb_pr:AB037733	+	1031.00	2072.63	4.4e+107	5139	! AB037733 Homo sapiens mRNA for
gb_pr:AF319857	+	1031.00	2071.45	5.1e+107	5080	! AX319857 Sequence 21 from Pate
gb_pr:AF261918	+	1025.00	2063.58	1.4e+106	3674	! AF261918 Homo sapiens disinteg
gb_pr:AX319858	+	655.00	1305.10	2.5e+64	4318	! AX319858 Sequence 22 from Pate
gb_1m:CEP13H10	-	590.00	1153.83	6.6e+56	3601	! 65361 Caenorhabditis elegans
gb_ro:D67076	+	562.50	1116.73	7.7e+54	4180	! D67076 Mouse mRNA for secretor
gb_pr:AF149118	+	562.50	1115.24	9.3e+54	4878	! AF149118 Rattus norvegicus a c
gb_pr:AF29966	+	559.00	1116.83	7.6e+54	2184	! E29966 Human ADAMTS-1 protein
gb_ro:AF304446	+	555.50	1106.07	3.0e+53	2873	! AF304446 Rattus norvegicus ADAM
gb_pr:AB58656	+	550.50	1095.86	1.1e+52	2853	! E58656 Novel metallic protease
gb_pr:AF060152	+	550.50	1094.09	1.4e+52	3030	! AF060152 Homo sapiens MEF1 pr
gb_pr:E29406	+	550.50	1092.58	1.7e+52	4014	! E29406 Novel integrin ligand
gb_pr:AB037767	+	550.50	1091.90	1.9e+52	4309	! AB037767 Homo sapiens mRNA for
gb_pr:AF170084	+	550.50	1091.60	1.9e+52	4447	! AF170084 Homo sapiens metallo
gb_pr:AF207664	+	550.50	1091.15	2.1e+52	4659	! AF207664 Homo sapiens matrix m
gb_pr:AX342635	+	519.50	1032.22	3.9e+49	2930	! AX342635 Sequence 32 from Pate
gb_pr:AX319860	+	513.00	1032.20	3.9e+49	739	! AX319860 Sequence 24 from Pate
gb_pr:AF175283	+	513.00	1022.16	4.0e+49	739	! AF175283 Homo sapiens zinc meta
gb_pr:AF060153	+	513.00	1016.66	2.9e+48	3711	! AF060153 Homo sapiens MET2 pr
gb_pr:AF5282	+	509.00	1011.90	5.8e+48	2670	! E5282 Novel metalloprotease
gb_pr:AF8655	+	509.00	1011.15	5.8e+48	2670	! AF207664 Homo sapiens matrix m
gb_pr:AX342635	+	503.00	996.41	3.9e+47	3638	! AX342635 Sequence 32 from Pate
gb_pr:HS4205725	+	490.00	995.55	1.8e+45	5115	! AJ250725 Homo sapiens zinc met
gb_pr:AF140675	+	489.00	969.08	1.3e+45	3119	! AF140675 Homo sapiens zinc met
gb_pr:AF5265	+	489.00	964.61	2.3e+45	5061	! E5265 Novel metalloprotease
gb_pr:AX128433	+	483.00	965.77	2.5e+45	1251	! AX128433 Sequence 2 from Pate
gb_pr:AB042271	+	483.00	965.77	2.8e+45	1251	! AB042271 Rattus norvegicus mRN
gb_pr:AF142813	+	482.00	952.11	1.1e+44	4193	! AF142813 Homo sapiens aggrecan
gb_pr:AF142099	+	482.00	951.86	1.2e+44	4301	! AB01588 Homo sapiens mRNA for
gb_pr:AF142099	+	460.50	911.36	2.1e+42	3002	! AF140673 Mus musculus putative
gb_pr:AF140674	+	459.50	909.82	2.6e+42	2843	! AF140674 Homo sapiens zinc met
gb_pr:AF142099	+	450.50	893.22	2.2e+41	5533	! AF142099 Homo sapiens aggrecan
gb_pr:AX327757	+	453.00	888.00	1.2e+41	2445	! AX327757 Sequence 13 from Pate
gb_pr:AF142271	+	453.00	885.62	1.6e+41	3132	! AX327754 Sequence 10 from Pate
gb_pr:AF142271	+	453.00	885.08	1.7e+41	3312	! E52775 Novel metalloprotease
gb_pr:AF142271	+	453.00	885.03	1.7e+41	3329	! AX327752 Sequence 8 from Pate
gb_pr:AF142271	+	453.00	884.63	1.8e+41	3471	! AX327755 Sequence 11 from Pate
gb_pr:AF142271	+	445.00	878.47	1.4e+40	3400	! AX327751 Sequence 15 from Pate
gb_pr:AF142271	+	439.50	866.48	6.7e+40	3675	! AX327752 Sequence 16 from Pate

GSWTPCSATCGKGJTRMRYSCRDENGSSVADESACATLPRPVAKKECSTVPGONKALD
WSSESVTCQSGRAUTQMCVNVDHVIDRSECDDYIPTPOODCSMSPCPORTPSSL
AQHQFQNEYRPRPASPERTHVGGNQRTGPGACSSTCAGSGDORVWCQDENGYT
ANDCVVERIFEDRACESCPOMAYGWGECKKLCOGGIRRLVVCORSNGERIFPD
SCETILDKPPDREOONTAHCPIHDAMSTPWSSSSVGGRHQRNTYCMARDGSILLES
DYCKHLAKPHGRKRGCRGCRPKWKAWSOCWSGCCGVDRHVGCOIGHKTAETE
CNPYKPESERDCGPRLITREREEQEQTICGEGSKRKKVVCDNNKNEWGAR
CDVSKEPVDRCSCLQPCVWLTGENSEVPSEL."

BASE COUNT ORIGIN 1471 a 1112 c 1362 g 1194 t

alignment_scores:
Quality: 1031.00 Length: 190
Ratio: 5.426 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
-09-972-467-2_COPY_289_478 x AB037733 ..

Align seg 1/1 to: AB037733 from: 1 to: 5139

1 LeuSerTyrProArgPheValLeuValLeuValAlaAspAspArgMet 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
392 TTAACTTACCCAGGTGTTAGAACGCTGGAGCACACAATGAAT 441

17 tvalSerTyrHisGlyGluAspLeuGlnHistylileLeuThrleuMetS 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
442 GGTTTCATACCAGGAGAAACTCTCACACTATTTACTTATGT 491

34 erileValAlaSerLeuTyrLysAspProSerIleGlyAsnLeuIleAsn 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
492 CAATTGACCTCTATCATATAAGGCCAGTAGTGAATTAAATTAAT 541

51 IleValLeuValAsnLeuLeuValLeuHisAsnGluGlnAspGlnProle 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
592 ATGGTTATGTCGACTTAATGGATCATATGAGCAGGATGGCCTTC 591

67 rileSerPheAsnAlaGlnIleGlyAsnLeuLysAsnProCysGlnTrpGlnH 84
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
592 CATATCTTAACTCTAGACACAACTAAACTTGCCAGTGGCAG 641

84 IsserlysasnSerProGlyGlyIleHisIleAspPheAlaValLeuLeu 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
642 ATTGGARGAACAGGCCAGGGATCACTCTCTCTCTCTCTCTCTCTCTA 691

101 ThraGlnGlnAspIleCysArgAlaHisAspLysProCysAspThrIleGly 117
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
692 ACAGAGCAGGATATCTGCAAGCTACGACAAATGTGATACTTCAGCT 741

117 ValAlaGluIleGlyIleIleGlyAspProTyroArgSerCysSerIleSerG 134
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
742 GGCTGACTTGACCTGACCATTTGACCCCTATAGCTATGT 791

134 IuAspSerGlyIleLeuSerThrAlaIleIleAlaIleGlyIle 150
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
792 AAGATAGTGGATTGAGTACAGCTTGTAGATGCCATGAGCAGGGCCAT 841

151 ValPheAsnMetProHisAspAspAsnAsnLysCysLysGluGlyIva 167
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
167 LysSerProGlnHisValMetAlaProThrLeuAsnDpheTyrThrAsnp 184
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
892 TAAGAGTCCCAAGGATGTCATGGCTCAACACTGGACTCTACCAACC 941

184 rotPheMetIleSerTyrScys 190
||||| ||||| ||||| ||||| |||||

942 CCTGGATGTCAGCTCAAGCT 961

AJ319857

Locus AX319857 Sequence 5808 bp DNA linear PAT 14-DEC-2001
Definition Sequence 21 from Patent WO0183782.
Accession AX319857
Version AX319857.1 GI:17901447
Keywords human.
Source Homo sapiens
Organism Homo sapiens; Mammalia; Butheria; Primates; Catarrhini; Homidae; Homo; Euksyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Plowman, G.D., Whyte, D., Sudarsanam, S., Manning, G., Caenepeel, S. and Payne, V.
Title Novel proteases
Journal Patent: WO 0183782-A 21-08-NOV-2001;
Features Source 1. -5808 /db/xref="Taxon 9606"
Title /Organism="Homo sapiens"
Journal Sugen, Inc. (US)
Source 1. -5808 /Location/Qualifiers
Base Count 1609 a 1354 c 1540 g 1305 t
Origin
Alignment_scores:
Quality: 1031.00 Length: 190
Ratio: 5.426 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-972-467-2_COPY_289_478 x AX319857 ..

Align seg 1/1 to: AX319857 from: 1 to: 5808

1 LeuSerTyrProArgPheValLeuValLeuValAlaAspAspArgMet 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
865 TTATCCCATCCAGGTTGAGTCAGTCTGTTGTTGGCAGACAGAT 914

17 tvalSerTyrHisGlyGlyAsnLeuGlnHistylileLeuThrLeuMetS 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
915 GTTTCATACATGGAGAACCTTCACACTATTTTACCTTATGT 964

34 erileValAlaSerLeuTyrLysAspProSerIleGlyAsnLeuIleAsn 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
965 CATGGCCCTCTATATAAGGCCAGTATGGAAATTATTAAT 1014

51 IleValLeuValAsnLeuLeuValLeuHisAsnGluGlnAspGlyProle 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1015 ATGGTTATGTCGACTTAATGGATCATATGCTATTCAGCT 1064

67 rileSerPheAsnAlaGlnIleIleLeuLysAsnProCysGlnTrpGlnH 84
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1065 CTATCTTATACGTCAGACAACTAAACTTGTGCTGCTGAGGAGC 1114

84 IsserlysasnSerProGlyGlyIleHisIleAspPheAlaValLeuLeu 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1115 ATTCGAGAGACGTCAGGTTGAACTCCATGATCTGCTGCTCTA 1164

101 ThraGlnAspIleCysArgAlaHisAspLysProCysAspThrIleGly 117
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1165 ACAGAGCAGGATATCTGCAAGCTACGACAAATGTGATACTTCAGCT 1214

117 ValAlaGluIleGlyIleIleLeuLysAspProTyroArgSerCysSerIleSerG 134
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1215 GCTGTAATGGACCTGATGTCATGAGCTTGTCTTGTCTTGTCTTGT 1264

134 IuAspSerGlyIleLeuSerThrAlaIleIleAlaIleGlyIle 150
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1265 AGATAGTGGATTGAGTACAGCTTGTAGATGCCATGAGCTGGCCAT 1314

151 ValPheAsnMetProHisAspAspAsnAsnLysCysLysGluGlyIva 167
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1315 GTGTTTACATGCCCTCATGAGACACACAACTGTAAGGAAGGAGT 1364

alignment_scores:

Quality: 422.00

Length: 70

Gaps: 0

Percent Similarity: 100.000
Ratio: 6.029
Percent Identity: 100.000

alignment_block:

US-09-972-467-2_COPY_509_578 x AF261918 ..

Align seq 1/1 to: AF261918 from: 1 to: 3674

1 GlneuproglileleutyrasnvalasnlyslnCysGluilephep 17

1537 CACTGCCAGGCATCCCTTACACGTAATAACATGATGATT 1586

17 egliprolyserglnvalcysprotrymetmeglnlysargargleut 34

1587 TGACCGAGTCAGGTGAGCCATATGATCAGTCAGGGCT 1636

34 rpvcsasnasnvalasnlyslslycysargtglnisthr 50

1637 GGNGCAATTAACGTCATGGAGTACAAGGCTCCGGACTCACACA 1686

51 ProtrplalaaspGlythrGlucysgluProlylshislysystyrgl 67

1687 CCCTGGCCGATGGACGGAGTGCGCCTGGAAAGCACTGCAAGTATGG 1736

67 YPheCysVal 70

1737 ATTTCGTT 1746

seq_name: gb_pt:AB037733

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